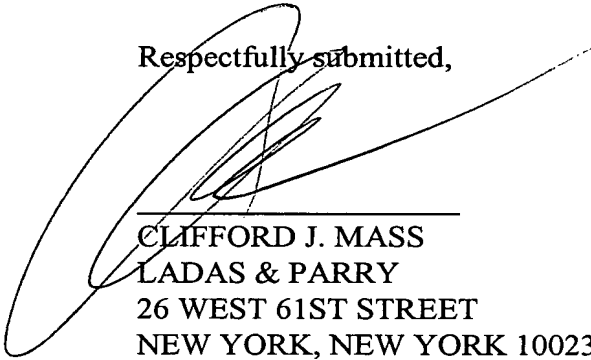


## REMARKS

The above amendatory action is taken in response to the Official Communication dated April 9, 2004. The Sequence Listing has been revised to correct the errors noted in the communication. Applicants submit herewith a paper copy and a computer readable form copy of the Sequence Listing and statements that the contents of the paper and computer readable form copies are the same and include no new matter.

Applicants have now complied with the requirements in the aforementioned Official Communication and respectfully request an early examination of this application on the merits.

Respectfully submitted,



\_\_\_\_\_  
CLIFFORD J. MASS  
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## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

(i) APPLICANT: Oon, Chong Jin  
Lim, Gek Keow  
Zhao, Yi  
Chen, Wei Ning

(ii) TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND  
USES THEREOF

(iii) NUMBER OF SEQUENCES: 11

#### (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Ladas & Parry  
(B) STREET: 26 West 61 Street  
(C) CITY: New York  
(D) STATE: New York  
(E) COUNTRY: USA  
(F) ZIP: 10023

#### (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

#### (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/719,528  
(B) FILING DATE: 19-DEC-2000  
(C) CLASSIFICATION: 435

#### (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/SG98/00046  
(B) FILING DATE: 19-JAN-1998

#### (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mass, Clifford J.  
(B) REGISTRATION NUMBER: 30,086  
(C) REFERENCE/DOCKET NUMBER: U-014987-0

#### (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 708-1800

### (2) INFORMATION FOR SEQ ID NO:1:

#### (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3215 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCCACAACA	TTCCACCAAG	CTCTGCTAGA	TCCCAGGGTG	AGGGGCCTAT	ATTTTCCTGC	60
TGGTGGCTCC	AGTTCCGGAA	CAGTAAACCC	TGTTCCGACT	ACTGCCTCTC	CCATATCGTC	120
AATCTTCTCG	AGGACTGGGG	ACCCTGCACC	GAACATGGAG	AACACAACAT	CAGGATTCCCT	180
AGGACCCCTG	CTCGTGTTAC	AGGCGGGGTT	TTTCTCGTTG	ACAAGAATCC	TCACAATACC	240
GCAGAGTCTA	GACTCTGGTG	GACTTCTCTC	AATTTTCTAG	GGGGAGCACC	CACGTGTTCC	300
TGGCCAAAAT	TCGCAGTCCC	CAACCTCCAA	TCACTCACCA	ACCTCTTGTC	CTCCAATTTG	360
TCCTGGCTAT	CGCTGGATGT	GTCTGCGGCG	TTTTATCATA	TTCTCTTTCA	TCCTGCTGCT	420
ATGCCTCATC	TTCTTGTTGG	TTCTTCTGGA	CTACCAAGGT	ATGTTGCCCG	TTTGTCTCTT	480
ACTTCCAGGA	ACATCAACCA	CCAGCACGGG	GCCATGCAAG	ACCTGCACGA	CTCCTGCTCA	540
AGGAAACTCT	ACGTTTCCCT	CTTGTTGCTG	TACAAAACCT	TCGGACGGAA	ACTGCACTTG	600
TATTCCCATC	CCATCATCCT	GGGCTTTTCG	AAGATTCCTA	TGGGAGTGGG	CCTCAGTCCG	660
TTTCTCCTGG	CTCAGTTTAC	TAGTGCCATT	TGTTCACTGG	TTCGTAGGGC	TTTCCCCCAC	720
TGTTTGGCTT	TCAGTTATAT	GGATGATGTG	GTATTGGGGG	CGAAGTCTGT	ACAACATCTT	780
GAGTCCCTTT	TTACCTCTAT	TACCAATTTT	CTTTTGTCTT	TGGGTATACA	TTTAAACCTT	840
AATAAAACCA	AACGTTGGGG	CTACTCCCTT	AACTTCATGG	GATATGTAAT	TGGAAGTTGG	900
GGTACTTTAC	CGCAGGAACA	TATTGTACTA	AAACTCAAGC	AATGTTTTTC	AAAACGCTT	960
GTAAATAGAC	CTATTGATTG	GAAAGTATGT	CAAAGAATTG	TGGGTCTTTT	GGGCTTTGCT	1020
GCCCCTTTTA	CACAATGTGG	CTATCCTGCC	TTGATGCCTT	TATATGCATG	TATACAATCT	1080
AAGCAGGCTT	TCACTTTCTC	GCCAACTTAC	AAGGCCTTTC	TGTGTAAACA	ATATCTGAAC	1140
CTTTACCCCG	TTGCCCGGCA	ACGGTCCGGT	CTCTGCCAAG	TGTTTGCTGA	CGCAACCCCC	1200
ACTGGATGGG	GCTTGGCCAT	AGGCCATCAG	CGCATGGCTG	GAACCTTTCT	GGCTCCTCTG	1260
CCGATCCATA	CTGCGGAACT	CCTAGCAGCT	TGTTTTGCTC	GCAGCCGGTC	TGGAGCAAAA	1320
CTTATCGGAA	CCGACAACCT	TGTTGTCCTC	TCTCGGAAAT	ACACCTCCTT	TCCATGGCTG	1380
CTAGGGTGTG	CTGCCAACTG	GATCCTGCGC	GGGACGTCCT	TTGTCTACGT	CCCGTCGGCG	1440
CTGAATCCCC	CGGACGACCC	GTCTCGGGGC	CGTTTGGGGC	TCTACCGTCC	CCTTCTTCAT	1500
CTGCCGTTCC	GGCCGACCAC	GGGGCGCACC	TCTCTTTACG	CGGTCTCCCC	GTATGTGCCT	1560
TCTCATCTGC	CGGACCGTGT	GCACTTCGCT	TCACCTCTGC	ACGTCGCATG	GAGACCACCG	1620
TGAACGCACG	CCAGGTCTTG	CCCAAGGTCT	TATATAAGAG	GACTCTTGGA	CTCTCAGCAA	1680
TGTCAACGAC	CGACCTTGAG	GCATACTTCA	AAGACTGTGT	GTTTAAAGAC	TGGGAGGAGT	1740

TGGGGGAGGA	GATTAGGTTA	AAGATTTATG	TACTAGGAGG	CTGTAGGCAT	AAATTGGTCT	1800
GTTCACCAGC	ACCATGCAAC	TTTTTCTCCT	CTGCCTAATC	ATCTCATGTT	CATGTCCTAC	1860
TGTTCAAGCC	TCCAAGCTGT	GCCTTGGGTG	GCTTTGGGAC	ATGGACATTG	ACCCGTATAA	1920
AGAATTTGGA	GCATCTGCTG	AGTTACTCTC	TTTTTTGCCT	TCTGACTTCT	TTCCGTCTAT	1980
TCGAGATCTC	CTCGACACCG	CCTCTGCTCT	GTATCGGGAG	GCCTTAGAGT	CTCCGGAACA	2040
TTGTTGCGCT	CACCATACAG	CACTCAGGCA	AGCTATTTTG	TGTTGGGGTG	AGTTGATGAA	2100
TCTGGCCACC	TGGGTGGGAA	GTAATTTGGA	AGATCCAGCA	TCCAGGGAAT	TAGTAGTCAG	2160
CTATGTCAAC	GTTAATATGG	GCCTAAAACT	CAGACAAATA	TTGTGGTTTC	ACATTTCTCTG	2220
TCTTACTTTT	GGAAGAGAAA	CTGTTCTTGA	GTACTTG GTA	TCTTTTGGAG	TGTGGATTCTG	2280
CACTCCTACC	GCTTACAGAC	CACCAAATGC	CCCTATCTTA	TCAACACTTC	CGGAAACTAC	2340
TGTTGTTAGA	CGACGAGGCA	GGTCCCCTAG	AAGAAGAACT	CCCTCGCCTC	GCAGACGAAG	2400
GTCTCAATCG	CCGCGTCGCA	GAAGATCTCA	ATCTCGGGAA	TCTCAACGTT	AGTATTCCTT	2460
GGACTCATAA	GGTGGGAAAC	TTTACTGGGC	TTTATTCTTC	TACTGTACCT	GTCTTTAATC	2520
CCGAGTGGCA	AATTCCTTCC	TTTCCTCACA	TTCAATTACA	AGAGGACATT	ATTAATAGAT	2580
GTCAACAATA	TGTGGGCCCT	CTTACAGTTA	ATGAAAAAAG	AAGATTAAAA	TTAATTATGC	2640
CTGCTAGGTT	TTATCCTAAC	CTTACTAAAT	ATTTGCCCTT	AGACAAAGGC	ATTAAACCGT	2700
ATTATCCTGA	ACATGCAGTT	AATCATTACT	TCAAACTAG	GCATTATTTA	CATACTCTGT	2760
GGAAGGCTGG	CATTCTATAT	AAGAGAGAAA	CTACACGCAG	CGCCTCATTT	TGTGGGTCAC	2820
CATATTCTTG	GGAACAAGAG	CTACAGCATG	GGAGGTTGGT	CTTCCAAACC	TCGACAAGGC	2880
ATGGGGAGCA	ATCTTGCTGT	TCCCAATCCT	CTGGGATTCT	TTCCCGATCA	CCAGTTGGAC	2940
CCTGCGTTTCG	GAGCCAACTC	AAACAATCCA	GATTGGGACT	TCAACCCCAA	CAAGGATCAC	3000
TGGCCAGAGG	CAAATCAGGT	AGGAGTGGGA	GCATTGCGGC	CAGGGTTCAC	CCCACCACAC	3060
GGCGGTCTTT	TGGGGGGGAG	CCCTCAGGCT	CAGGGCATAT	TGACAACAGT	GCCAGCAGCA	3120
CCTCCTCCTG	CCTCCACCAA	TCGGCAGTCA	GGAAGACAGC	CTACTCCCAT	CTCTCCACCT	3180
CTAAGAGACA	GTCATCCTCA	GGCCACGCAG	TGGAA			3215

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 843 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Pro	Leu	Ser	Tyr	Gln	His	Phe	Arg	Lys	Leu	Leu	Leu	Leu	Asp	Asp	1	5	10	15
Glu	Ala	Gly	Pro	Leu	Glu	Glu	Glu	Leu	Pro	Arg	Leu	Ala	Asp	Glu	Gly	20	25	30	
Leu	Asn	Arg	Arg	Val	Ala	Glu	Asp	Leu	Asn	Leu	Gly	Asn	Leu	Asn	Val	35	40	45	
Ser	Ile	Pro	Trp	Thr	His	Lys	Val	Gly	Asn	Phe	Thr	Gly	Leu	Tyr	Ser	50	55	60	
Ser	Thr	Val	Pro	Val	Phe	Asn	Pro	Glu	Trp	Gln	Ile	Pro	Ser	Phe	Pro	65	70	75	80
His	Ile	His	Leu	Gln	Glu	Asp	Ile	Ile	Asn	Arg	Cys	Gln	Gln	Tyr	Val	85	90	95	
Gly	Pro	Leu	Thr	Val	Asn	Glu	Lys	Arg	Arg	Leu	Lys	Leu	Ile	Met	Pro	100	105	110	
Ala	Arg	Phe	Tyr	Pro	Asn	Leu	Thr	Lys	Tyr	Leu	Pro	Leu	Asp	Lys	Gly	115	120	125	
Ile	Lys	Pro	Tyr	Tyr	Pro	Glu	His	Ala	Val	Asn	His	Tyr	Phe	Lys	Thr	130	135	140	
Arg	His	Tyr	Leu	His	Thr	Leu	Trp	Lys	Ala	Gly	Ile	Leu	Tyr	Lys	Arg	145	150	155	160
Glu	Thr	Thr	Arg	Ser	Ala	Ser	Phe	Cys	Gly	Ser	Pro	Tyr	Ser	Trp	Glu	165	170	175	
Gln	Glu	Leu	Gln	His	Gly	Arg	Leu	Val	Phe	Gln	Thr	Ser	Thr	Arg	His	180	185	190	
Gly	Asp	Glu	Ser	Cys	Cys	Ser	Gln	Ser	Ser	Gly	Ile	Leu	Ser	Arg	Ser	195	200	205	
Pro	Val	Gly	Pro	Cys	Val	Arg	Ser	Gln	Leu	Lys	Gln	Ser	Arg	Leu	Gly	210	215	220	
Leu	Gln	Pro	Gln	Gln	Gly	Ser	Leu	Ala	Arg	Gly	Lys	Ser	Gly	Arg	Ser	225	230	235	240
Gly	Ser	Ile	Arg	Ala	Arg	Val	His	Pro	Thr	Thr	Arg	Arg	Ser	Phe	Gly	245	250	255	
Gly	Glu	Pro	Ser	Gly	Ser	Gly	His	Ile	Asp	Asn	Ser	Ala	Ser	Ser	Thr	260	265	270	

Ser Ser Cys Leu His Gln Ser Ala Val Arg Lys Thr Ala Tyr Ser His  
 275 280 285  
 Leu Ser Thr Ser Lys Arg Gln Ser Ser Ser Gly His Ala Val Glu Leu  
 290 295 300  
 His Asn Ile Pro Pro Ser Ser Ala Arg Ser Gln Gly Glu Gly Pro Ile  
 305 310 315 320  
 Phe Ser Cys Trp Trp Leu Gln Phe Arg Asn Ser Lys Pro Cys Ser Asp  
 325 330 335  
 Tyr Cys Leu Ser His Ile Val Asn Leu Leu Glu Asp Trp Gly Pro Cys  
 340 345 350  
 Thr Glu His Gly Glu His Asn Ile Arg Ile Pro Arg Thr Pro Ala Arg  
 355 360 365  
 Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn Pro His Asn Thr Ala  
 370 375 380  
 Glu Ser Arg Leu Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro  
 385 390 395 400  
 Thr Cys Ser Trp Pro Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr  
 405 410 415  
 Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala  
 420 425 430  
 Ala Phe Tyr His Ile Pro Leu His Pro Ala Ala Met Pro His Leu Leu  
 435 440 445  
 Val Gly Ser Ser Gly Leu Pro Arg Tyr Val Ala Arg Leu Ser Ser Thr  
 450 455 460  
 Ser Arg Asn Ile Asn His Gln His Gly Ala Met Gln Asp Leu His Asp  
 465 470 475 480  
 Ser Cys Ser Arg Lys Leu Tyr Val Ser Leu Leu Leu Leu Tyr Lys Thr  
 485 490 495  
 Phe Gly Arg Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe  
 500 505 510  
 Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln  
 515 520 525  
 Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro His Cys  
 530 535 540  
 Leu Ala Phe Ser Tyr Met Asp Asp Val Val Leu Gly Ala Lys Ser Val  
 545 550 555 560  
 Gln His Leu Glu Ser Leu Phe Thr Ser Ile Thr Asn Phe Leu Leu Ser  
 565 570 575

Leu	Gly	Ile	His	Leu	Asn	Pro	Asn	Lys	Thr	Lys	Arg	Trp	Gly	Tyr	Ser		
			580					585					590				
Leu	Asn	Phe	Met	Gly	Tyr	Val	Ile	Gly	Ser	Trp	Gly	Thr	Leu	Pro	Gln		
		595					600					605					
Glu	His	Ile	Val	Leu	Lys	Leu	Lys	Gln	Cys	Phe	Arg	Lys	Leu	Pro	Val		
	610					615					620						
Asn	Arg	Pro	Ile	Asp	Trp	Lys	Val	Cys	Gln	Arg	Ile	Val	Gly	Leu	Leu		
625					630					635					640		
Gly	Phe	Ala	Ala	Pro	Phe	Thr	Gln	Cys	Gly	Tyr	Pro	Ala	Leu	Met	Pro		
				645					650					655			
Leu	Tyr	Ala	Cys	Ile	Gln	Ser	Lys	Gln	Ala	Phe	Thr	Phe	Ser	Pro	Thr		
			660					665					670				
Tyr	Lys	Ala	Phe	Leu	Cys	Lys	Gln	Tyr	Leu	Asn	Leu	Tyr	Pro	Val	Ala		
	675						680					685					
Arg	Gln	Arg	Ser	Gly	Leu	Cys	Gln	Val	Phe	Ala	Asp	Ala	Thr	Pro	Thr		
	690					695					700						
Gly	Trp	Gly	Leu	Ala	Ile	Gly	His	Gln	Arg	Met	Ala	Gly	Thr	Phe	Leu		
705					710					715					720		
Ala	Pro	Leu	Pro	Ile	His	Thr	Ala	Glu	Leu	Leu	Ala	Ala	Cys	Phe	Ala		
				725					730				735				
Arg	Ser	Arg	Ser	Gly	Ala	Lys	Leu	Ile	Gly	Thr	Asp	Asn	Ser	Val	Val		
			740					745					750				
Leu	Ser	Arg	Lys	Tyr	Thr	Ser	Phe	Pro	Trp	Leu	Leu	Gly	Cys	Ala	Ala		
	755						760					765					
Asn	Trp	Ile	Leu	Arg	Gly	Thr	Ser	Phe	Val	Tyr	Val	Pro	Ser	Ala	Leu		
	770					775					780						
Asn	Pro	Ala	Asp	Asp	Pro	Ser	Arg	Gly	Arg	Leu	Gly	Leu	Tyr	Arg	Pro		
785					790					795					800		
Leu	Leu	His	Leu	Pro	Phe	Arg	Pro	Thr	Thr	Gly	Arg	Thr	Ser	Leu	Tyr		
				805					810					815			
Ala	Val	Ser	Pro	Tyr	Val	Pro	Ser	His	Leu	Pro	Asp	Arg	Val	His	Phe		
			820					825					830				
Ala	Ser	Pro	Leu	His	Val	Ala	Trp	Arg	Pro	Pro							
		835					840										

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 400 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Gly	Gly	Trp	Ser	Ser	Lys	Pro	Arg	Gln	Gly	Met	Gly	Thr	Asn	Leu	1	5	10	15
Ala	Val	Pro	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro	20	25	30	
Ala	Phe	Gly	Ala	Asn	Ser	Asn	Asn	Pro	Asp	Trp	Asp	Phe	Asn	Pro	Asn	35	40	45	
Lys	Asp	His	Trp	Pro	Glu	Ala	Asn	Gln	Val	Gly	Val	Gly	Ala	Phe	Gly	50	55	60	
Pro	Gly	Phe	Thr	Pro	Pro	His	Gly	Gly	Leu	Leu	Gly	Gly	Ser	Pro	Gln	65	70	75	80
Ala	Gln	Gly	Ile	Leu	Thr	Thr	Val	Pro	Ala	Ala	Pro	Pro	Pro	Ala	Ser	85	90	95	
Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro	Ile	Ser	Pro	Pro	Leu	100	105	110	
Arg	Asp	Ser	His	Pro	Gln	Ala	Thr	Gln	Trp	Asn	Ser	Thr	Thr	Phe	His	115	120	125	
Gln	Ala	Leu	Leu	Asp	Pro	Arg	Val	Arg	Gly	Leu	Tyr	Phe	Pro	Ala	Gly	130	135	140	
Gly	Ser	Ser	Ser	Gly	Thr	Val	Asn	Pro	Val	Pro	Thr	Thr	Ala	Ser	Pro	145	150	155	160
Ile	Ser	Ser	Ile	Phe	Ser	Arg	Thr	Gly	Asp	Pro	Ala	Pro	Asn	Met	Glu	165	170	175	
Asn	Thr	Thr	Ser	Gly	Phe	Leu	Gly	Pro	Leu	Leu	Val	Leu	Gln	Ala	Gly	180	185	190	
Phe	Phe	Ser	Leu	Thr	Arg	Ile	Leu	Thr	Ile	Pro	Gln	Ser	Leu	Asp	Ser	195	200	205	
Trp	Trp	Thr	Ser	Leu	Asn	Phe	Leu	Gly	Gly	Ala	Pro	Thr	Cys	Pro	Gly	210	215	220	
Gln	Asn	Ser	Gln	Ser	Pro	Thr	Ser	Asn	His	Ser	Pro	Thr	Ser	Cys	Pro	225	230	235	240
Pro	Ile	Cys	Pro	Gly	Tyr	Arg	Trp	Asn	Cys	Leu	Arg	Arg	Phe	Ile	Ile	245	250	255	
Phe	Leu	Phe	Ile	Leu	Leu	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu	260	265	270	



Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser  
 275 280 285  
 Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Thr Pro Ala Gln Gly  
 290 295 300  
 Asn Ser Thr Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn  
 305 310 315 320  
 Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu  
 325 330 335  
 Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro  
 340 345 350  
 Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val  
 355 360 365  
 Ile Trp Met Met Trp Tyr Trp Gly Arg Ser Leu Tyr Asn Ile Leu Ser  
 370 375 380  
 Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile  
 385 390 395 400

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gln Leu Phe Leu Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr  
 1 5 10 15  
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp Ile  
 20 25 30  
 Asp Pro Tyr Lys Glu Phe Gly Ala Ser Ala Glu Leu Leu Ser Phe Leu  
 35 40 45  
 Pro Ser Asp Phe Phe Pro Ser Ile Arg Asp Leu Leu Asp Thr Ala Ser  
 50 55 60  
 Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His  
 65 70 75 80  
 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Asn  
 85 90 95  
 Leu Ala Thr Trp Val Gly Ser Asn Leu Glu Asp Pro Ala Ser Arg Glu  
 100 105 110

Leu Val Val Ser Tyr Val Asn Val Asn Met Gly Leu Lys Leu Arg Gln  
 115 120 125  
 Ile Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val  
 130 135 140  
 Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Thr Ala  
 145 150 155 160  
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr  
 165 170 175  
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro  
 180 185 190  
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg  
 195 200 205  
 Glu Ser Gln Arg  
 210

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 154 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Ala Arg Val Cys Cys Gln Leu Asp Pro Ala Arg Asp Val Leu  
 1 5 10 15  
 Cys Leu Arg Pro Val Gly Ala Glu Ser Arg Gly Arg Pro Val Ser Gly  
 20 25 30  
 Pro Phe Gly Ala Leu Pro Ser Pro Ser Ser Ser Ala Val Pro Ala Asp  
 35 40 45  
 His Gly Ala His Leu Ser Leu Arg Gly Leu Pro Val Cys Ala Phe Ser  
 50 55 60  
 Ser Ala Gly Pro Cys Ala Leu Arg Phe Thr Ser Ala Arg Arg Met Glu  
 65 70 75 80  
 Thr Thr Val Asn Ala Arg Gln Val Leu Pro Lys Val Leu Tyr Lys Arg  
 85 90 95  
 Thr Leu Gly Leu Ser Ala Met Ser Thr Thr Asp Leu Glu Ala Tyr Phe  
 100 105 110  
 Lys Asp Cys Val Phe Lys Asp Trp Glu Glu Leu Gly Glu Glu Ile Arg  
 115 120 125

Leu Lys Ile Tyr Val Leu Gly Gly Cys Arg His Lys Leu Val Cys Ser  
 130 135 140  
 Pro Ala Pro Cys Asn Phe Phe Ser Ser Ala  
 145 150

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATAAGCTTAT GCCCCTATCT TATCAACACT TCCGGA 36

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGTCTAGAC TCTGCGGTAT TGTGA 25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCTAGAC TCGTGGTGGA CTTCT 25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGAGAATTCT CACGGTGGTC TCCATGCGAC GT

32

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTGTTTACG TCCCGT

16

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATAAGCTTAT GCCCCTATCT TATCAACACT TCCGGA

36